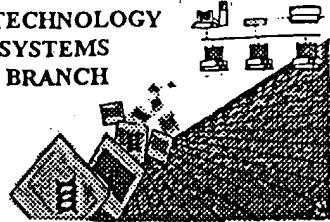


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/920,137B
Source: IPW
Date Processed by STIC: 10/1/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/920,137 B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 **Wrapped Nucleic** **Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was received in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 **Misaligned Amino Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 **Non-ASCII**

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 **Variable Length**

Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing

6 **PatentIn 2.0 "bug"**

A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.

7 **Skipped Sequences (OLD RULES)**

Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
 (2) INFORMATION FOR SEQ ID NO: X (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
 (ii) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences

8 **Skipped Sequences (NEW RULES)**

Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
 <210> sequence id number
 <400> sequence id number
 000

9 **Use of n's or Xaa's (NEW RULES)**

Use of n's and/or Xaa's have been detected in the Sequence Listing
 Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 **Invalid <213> Response**

Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or is Artificial Sequence

11 **Use of <220>**

Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 **PatentIn 2.0 "bug"**

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 **Misuse of n/Xaa**

"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/920,137B

DATE: 10/01/2004

TIME: 10:46:27

Input Set : A:\Cen 0250 SEQ LIST 07-09-01.txt
 Output Set: N:\CRF4\10012004\I920137B.raw

5 <110> APPLICANT: Giles-Komar, Jill
 6 David Shealy
 7 David Knight
 8 Bernie Scallion
 9 George Heavner
 11 <120> TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
 13 <130> FILE REFERENCE: CEN0250
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/920,137B
 C--> 15 <141> CURRENT FILING DATE: 2001-08-01
 15 <160> NUMBER OF SEQ ID NOS: 15
 17 <170> SOFTWARE: PatentIn Ver 3.1

ERRORED SEQUENCES

19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 5
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Homo sapiens
 W--> 23 <400> SEQUENCE: 1
 25 Arg Tyr Thr Met His
 E--> 26 1 ~~x~~ 5 ~~x~~
 28 <210> SEQ ID NO: 2
 29 <211> LENGTH: 17
 30 <212> TYPE: PRT
 31 <213> ORGANISM: Homo sapiens
 W--> 32 <400> SEQUENCE: 2
 34 Val Ile Ser. Phe. Asp Gly Ser Asn Lys Tyr Tyr Val Asp Ser Val Lys
 E--> 35 1 ~~x~~ 5 ~~x~~ 10 10 15 ~~x~~
 37 <210> SEQ ID NO: 3
 38 <211> LENGTH: 10
 39 <212> TYPE: PRT
 40 <213> ORGANISM: Homo sapiens
 W--> 41 <400> SEQUENCE: 3
 43 Glu Ala Arg Gly Ser Tyr Ala Phe Asp Ile
 E--> 44 1 ~~x~~ 5 ~~x~~ 10 ~~x~~
 64 <210> SEQ ID NO: 6
 65 <211> LENGTH: 10
 66 <212> TYPE: PRT
 67 <213> ORGANISM: Homo sapiens
 W--> 68 <400> SEQUENCE: 6
 70 Gln Gln Arg Ser Asn Trp Pro Pro Phe Thr
 E--> 71 1 ~~x~~ 5 5 10 ~~x~~

Does Not Contain
Corrected Diskette Needed

(PS-1-3)

Pls see item
3 on error
summary
sheet.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/920,137B

DATE: 10/01/2004

TIME: 10:46:27

Input Set : A:\Cen 0250 SEQ LIST 07-09-01.txt
Output Set: N:\CRF4\10012004\I920137B.raw

192 <210> SEQ ID NO: 13
193 <211> LENGTH: 32 *Found 42*
194 <212> TYPE: DNA
195 <213> ORGANISM: Homo sapiens
W--> 196 <400> SEQUENCE: 13
E--> 198 ctctcctgca gggccagtca gagtgtagc agtacttag cc

32 *42*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/920,137B

DATE: 10/01/2004

TIME: 10:46:28

Input Set : A:\Cen 0250 SEQ LIST 07-09-01.txt
Output Set: N:\CRF4\10012004\I920137B.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:23 M:283 W: Missing Blank Line separator, <400> field identifier
L:26 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1 ✓
L:32 M:283 W: Missing Blank Line separator, <400> field identifier
L:35 M:252 E: No. of Seq. differs, <211> LENGTH:Input:17 Found:16 SEQ:2 ✓
L:41 M:283 W: Missing Blank Line separator, <400> field identifier
L:44 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3 ✓
L:50 M:283 W: Missing Blank Line separator, <400> field identifier
L:59 M:283 W: Missing Blank Line separator, <400> field identifier
L:68 M:283 W: Missing Blank Line separator, <400> field identifier
L:71 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6 ✓
L:77 M:283 W: Missing Blank Line separator, <400> field identifier
L:108 M:283 W: Missing Blank Line separator, <400> field identifier
L:136 M:283 W: Missing Blank Line separator, <400> field identifier
L:172 M:283 W: Missing Blank Line separator, <400> field identifier
L:180 M:283 W: Missing Blank Line separator, <400> field identifier
L:188 M:283 W: Missing Blank Line separator, <400> field identifier
L:196 M:283 W: Missing Blank Line separator, <400> field identifier
L:198 M:254 E: No. of Bases conflict, LENGTH:Input:32 Counted:42 SEQ:13 ✓
L:198 M:252 E: No. of Seq. differs, <211> LENGTH:Input:32 Found:42 SEQ:13 ✓
L:204 M:283 W: Missing Blank Line separator, <400> field identifier
L:212 M:283 W: Missing Blank Line separator, <400> field identifier